

Molecular characterization of a novel human PDZ domain protein with homology to INAD from *Drosophila melanogaster*

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Abstract PDZ domains are thought to act as protein-binding modules mediating the clustering of membrane and membrane-associated proteins. The INAD protein has been shown to interact via a PDZ domain with the calcium channel TRP which contributes to capacitative calcium entry into *Drosophila* photoreceptor cells. We have cloned the cDNA of a human INAD-like protein (hINADL) of 1524 amino acids in length containing at least five PDZ domains. Additionally, two truncated versions hINADL_{Δ304} and hINADL_{Δ853} were identified. hINADL transcripts of differing size are expressed in various tissues including brain, where transcripts are abundant in the cerebellum.

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Key words: PDZ domain; INAD; GLGF repeat; Capacitative calcium entry; Membrane protein cluster; DHR domain

1. Introduction

PDZ domains have been identified in a rapidly expanding number of intracellular proteins. These approximately 100 amino acid domains were originally found in a family of proteins comprising the Postsynaptic density protein (PSD-95, [1]/SAP90, [2]), the Disc-large tumor suppressor (dlg, [3]) and the Zonula occludens protein (ZO-1, [4]) which are located at synaptic, septate or tight junctions, respectively. These PDZ proteins are characterized by the presence of several PDZ domains, an additional Src homology domain (SH3) and a modified guanylate kinase domain (GUK) and are combined as a subclass of the membrane-associated guanylate kinases (MAGUK, reviewed in [5]). The PDZ amino acid sequence motif could be detected in further proteins of yet unknown function, in the dystrophin-associated syntrophins [6] and in the family of protein tyrosine phosphatases (PTP, [7,8]), which possess an additional phosphatase domain and a band 4.1-like region.

PDZ domains are also known as Discs-large Homology Repeats (DHR) or GLGF repeats, according to the presence of a GLGF amino acid motif. They represent protein binding domains which mediate the interaction to their binding partners by at least two mechanisms. First, they bind to specific amino acid motifs located at the very C-terminal end of the target proteins. As shown for example for the interaction of the second PDZ domain of PSD-95 and the ionotropic

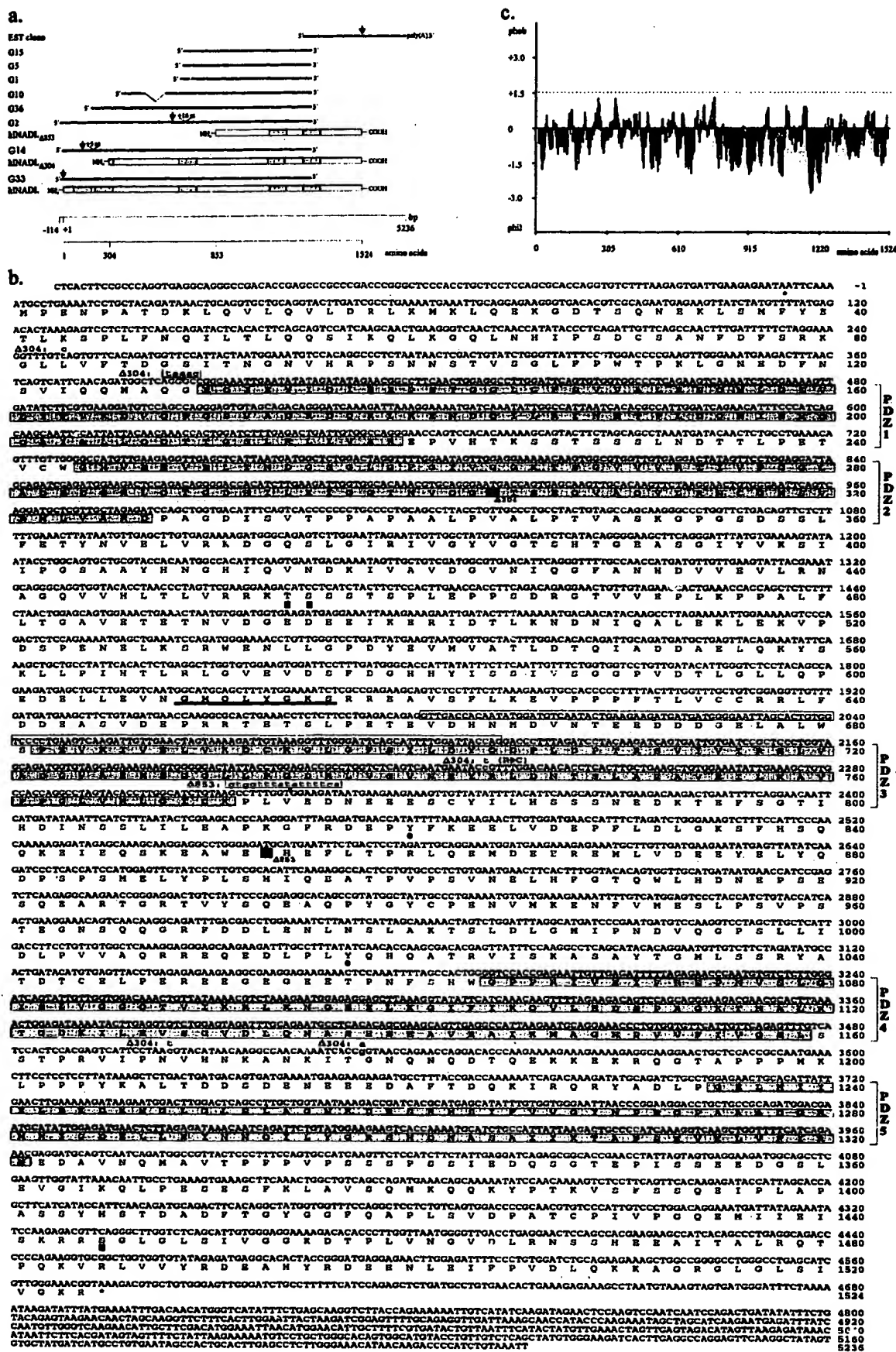
NMDA receptor [9] or the shaker type potassium channel [10] this C-terminal amino acid motif consists of a serine or a threonine residue followed by any amino acid and a valine residue (consensus S/TXV). Second, different proteins are able to interact via their PDZ domains and build heterodimers. Accordingly, the second PDZ domain of PSD-95 bind directly to the PDZ domain of the neuronal nitric oxide synthase [11]. Thus, the same the PDZ domain can bind target proteins in two different ways.

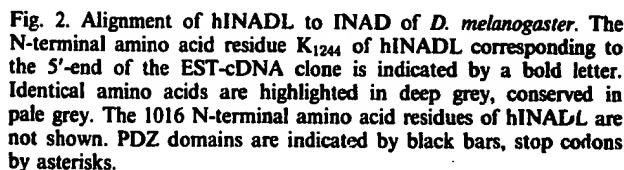
Interaction of PDZ proteins to their target molecules play a role in clustering proteins to specific locations at the plasma membrane. In this model PDZ proteins mediate cytoskeletal anchoring of membrane or membrane-associated proteins of which the proper function depend on the specific location and/or the vicinity of other regulatory components. Thus, PDZ proteins contribute to the formation of macromolecular complexes but may have also indirect or direct regulatory influence on the function of their target proteins.

The inactivation no after-potential C (*InaD*) mutation in *Drosophila melanogaster* affect the visual transduction in the compound eye of the fly. As reported by Shieh and Niemeyer [12] the *Drosophila InaD* gene (*dInaD*) encode a hydrophilic protein with two amino acid repeats that share sequence similarity to the PDZ domains of the MAGUK family. Recently, it could be shown that a PDZ domain of dINAD bind to the C-terminally located STV amino acid residues of the TRP calcium channel [13], which is thought to be involved in capacitative calcium entry (CCE). The association of dINAD and TRP is prevented by a point mutation in the *InaD* mutant that converts a methionine residue located in the second PDZ domain to a lysine. These findings have led to the suggestion that dINAD is a regulatory subunit of the TRP channel. Similarly, the INAD protein of *Calliphora vicina* (cINAD) interacts with *Calliphora* TRP and additionally with phospholipase C, the key enzyme of the inositol(1,4,5)trisphosphate (InsP₃)-cascade [14]. These three proteins and an eye specific protein kinase C seem to build a multimeric signalling complex. A structural significance of dINAD is obvious by the fact that INAD deficient *Drosophila* mutants undergo retinal degradation probably due to the lack of the TRP-INAD interaction [15].

Similar to INAD the TRP protein was identified as a mutation affecting the phototransduction in *Drosophila*. The lack of TRP led to a transient receptor potential due to the defect in light-induced Ca²⁺ entry across the membrane. Functional analysis of TRP showed that it is a Ca²⁺ channel which is activated following Ca²⁺ release from internal stores upon stimulation of the InsP₃ cascade [16–18]). We have cloned the cDNA of two capacitative calcium entry channels CCE1 [19] and CCE2 [20] from mammals. Both mammalian proteins possess significant amino acid identity to TRP [21] and also

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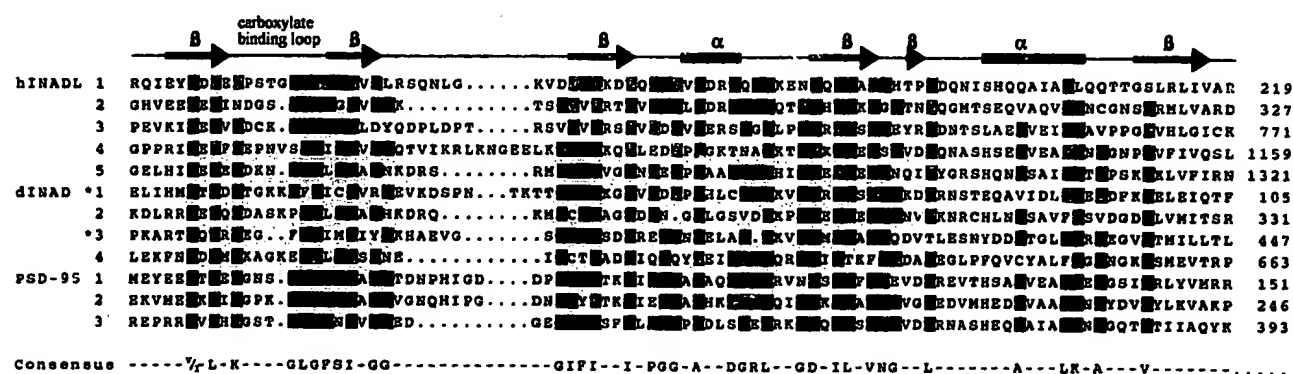


Fig. 3. Alignment of PDZ domains of hINADL, dINAD and PSD95. Amino acid residues are numbered on the right. A consensus sequence is given below for residues with a minimal frequency of 50% which are highlighted in deep grey. Conserved amino acids corresponding to the consensus sequence are shown in pale grey. The PDZ domains in dINAD originally identified by Shieh and Niemeyer [13] are signed by asterisks. The secondary structure elements predicted for the third PDZ domain of PSD-95 [31] are shown by arrows (β sheet), bars (α helix) and lines (connecting loops).

ilarity with the dINAD protein sequence. The first amino acid residue encoded by the 5'-cDNA sequence of the EST clone corresponds to D₂₅₅ of dINAD indicating that the EST protein is homologous to the C-terminal region of dINAD but lacks the N-terminus. To get the full-length cDNA sequence, we constructed a primer extension cDNA library using a specific primer derived from the 5'-region of the EST sequence and poly(A)⁺ RNA from human Girardi cells as template for the first-strand synthesis. 8×10^6 transformants were probed and 8 of more than 100 positive signals were analysed (Fig. 1a). All clones isolated contained the 5'-region of the EST clone comprising 74 bp. Three of the clones obtained, G2, G14 and G33, contained an in frame ATG triplet that appears downstream of a stop codon.

The 5350 nt cDNA sequence derived from clone G33 and the EST clone contained an open reading frame encoding a sequence of 1524 amino acids with a calculated molecular mass of 167358. Sequence analysis revealed that this protein which is called human INAD-like (hINADL), contains at least five PDZ domains assigned as PDZ1 to PDZ5 (Fig. 1). Two clones, G2 and G14, which are of similar length as clone G33, possess insertions of 5 and 16 nucleotides, respectively (Fig. 1a) leading to shifts in the reading frame and the ap-

pearance of other in frame stop codons upstream of ATG triplets. As a consequence, Met³⁰⁴ and Met⁸⁵³ are assigned as the translation initiation sites in G2 and G14, respectively. The resulting proteins hINADL_{Δ304} and hINADL_{Δ853} comprise 1221 and 672 amino acids (Fig. 1). The truncation of the N-terminus leads to the absence of two (hINADL_{Δ304}) or three (hINADL_{Δ853}) PDZ domains, respectively. hINADL appears to be the most abundant isoform expressed in Girardi cells because all other clones which were analysed correspond to G33 and do not contain the insertions detected in G2 and G14. A hydropathy analysis [30] of the amino acid sequence of hINADL (Fig. 1c) reveals the absence of a typical membrane spanning region. Additionally, the N-terminal sequence does not resemble a hydrophobic signal sequence. These properties are consistent with the assumption that hINADL is a hydrophilic protein which is not an integral part of the cell membrane but might be associated with intracellular domains of membrane proteins.

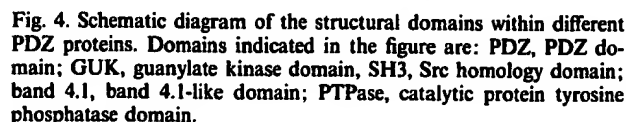
3.2. Sequence and structural similarities

A close inspection of the hINADL sequence reveals the presence of five PDZ domains with a length between 84 and 96 amino acids (Fig. 1b) covering amino acids 130-219, 244-

Table 1
Amino acid sequence similarity and identity of different members of the PDZ family

	hINADL	dINAD	PSD-95	SAP97	SAP102	DLG	ZO-1	SNT B1	Chapsyn	PTP1E
hINADL		52.3	50.7	46.4	50.1	45.2	40.7	43.7	47.4	46.7
dINAD	27.1		43.9	41.4	40.2	41.7	44.4	40.1	43.8	45.5
PSD-95	28.2	21.1		86.3	82.2	76.2	55.0	45.3	84.7	48.2
SAP97	21.6	18.8	74.2		78.5	75.7	46.5	44.6	74.8	48.3
SAP102	24.6	19.6	67.6	66.4		75.7	46.3	45.3	82.2	49.0
DLG	21.7	18.4	58.3	60.9	59.8		46.9	43.6	72.5	43.4
ZO-1	19.6	20.8	31.1	25.1	25.0	26.2		43.1	50.8	41.5
SNT B1	20.6	18.4	22.0	24.1	23.2	21.4	18.9		44.6	41.0
chapsyn	24.8	19.1	70.7	86.2	69.4	57.0	28.0	20.5		44.7
PTP1E	23.6	22.5	24.6	24.8	25.6	22.7	19.8	20.8	22.6	

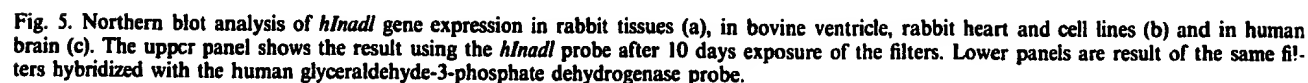
The amino acid sequences were aligned using the BestFit program and the local homology algorithm of Smith and Waterman [1]. GenBank accession numbers: dINAD (drosophila), U15803; PSD-95 (rat), M96853; SAP97 (rat), U14950; SAP102 (rat), U50147; DLG (drosophila), M73529; ZO1 (human), L14837; beta1-syntrophin (SNT B1, human), L31529; PTP1E (human), U12128.



The deduced amino acid sequence of hINADL is considerably longer than the sequence of dINAD. Nevertheless, the sequence of the dipterian protein possess significant sequence similarity to hINADL with only a few gaps and it is obvious

3.3. Tissue distribution of *hInadl* mRNA

Northern blot analysis shows that transcripts of about 9.0, 5.4, 4.1 and 1.5 kb are abundant in adrenal gland, kidney, ureter (Fig. 4a), heart and epithelial Girardi cells (Fig. 4b). Lower amounts of the transcripts are also present in other tissues including testis, lung (Fig. 4a), medulla and spinal cord (Fig. 4c). The 5.4 kb transcript, most prominent in human mRNA from cerebellum and Girardi cells correspond to the size of the cloned hINADL cDNA (5350 bp). The 9.0 kb transcripts and the less abundant and smaller mRNAs may differ in the 5'-untranslated sequence as a result of alternative mRNA processing. Alternatively, these signals may represent



rabbit, bovine and human mRNAs which are similar but not identical to hINADL (Fig. 5a,b).

4. Discussion

This study describes the molecular characterization of a novel human protein, hINADL, which contains at least five amino acid repeats which could be characterized as PDZ domains. Like other PDZ proteins including dipterian INAD, hINADL is hydrophilic and might contribute to clustering of membrane proteins. Sequence comparison of hINADL reveals significant similarity to INAD of *Drosophila* suggesting that hINADL represents the human homolog of dINAD. Although similarities to other PDZ proteins are obvious, hINADL as well as dINAD lack significant structural features of these proteins like guanylate kinase or protein tyrosine phosphatase domains. A major difference of the two proteins is their length. hINADL comprises 1524 amino acid residues whereas the dipterian INAD proteins are considerably smaller (674 and 665 amino acids) and in this respect resemble the N-terminally truncated isoforms hINADL Δ 853 and hINADL Δ 304. As shown for other PDZ proteins, hINADL may form multimeric complexes and interact with the carboxyl terminus of unrelated membrane proteins via its PDZ domains and thereby contribute to macromolecular complex formation within the cell membrane. Ongoing expression experiments will show whether — in analogy to the INAD/TRP interaction in the *Drosophila* compound eye — mammalian capacitative calcium entry channels like CCE1, CCE2 and other mammalian TRP homologs could be the molecular targets of hINADL. This is supported by the similarity of the tissue specific expression pattern of hINADL and CCE1/CCE2 [19,20]. Apparently, the C-terminal five amino acid residues in CCE1 and CCE2 might contribute to the interaction to hINADL. They comprise the amino acid motif TXL resembling the known interaction site of other PDZ domains S/TXV.

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